

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER

GJE-70

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

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097868352

INTERNATIONAL APPLICATION NO.
PCT/GB99/04377

INTERNATIONAL FILING DATE
22 Dec 1999

PRIORITY DATE CLAIMED
22 Dec 1998 (see no. 20 below)

TITLE OF INVENTION

Genes And Proteins, And Their Use

APPLICANT(S) FOR DO/EO/US Martin John Glenton Hughes, Joseph David Santangelo, Jonathan Douglas Lane, Robert Feldman, Joanne Christine Moore, Richard James Dobson, Paul Everest, Gordon Dougan, Rebecca Kerry Wilson

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include items (5), (6), (9) and (21) indicated below.
4. ☐ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is attached hereto (required only if not communicated by the International Bureau).
 - b. ☒ has been communicated by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. ☐ is attached hereto.
 - b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are attached hereto (required only if not communicated by the International Bureau).
 - b. ☐ have been communicated by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☐ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). unsigned.
10. ☐ An English language translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11 to 20 below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
14. ☐ A SECOND or SUBSEQUENT preliminary amendment.
15. ☐ A substitute specification.
16. ☐ A change of power of attorney and/or address letter.
17. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 37 CFR 1.821 - 1.825.
18. ☐ A second copy of the published international application under 35 U.S.C. 154(d)(4).
19. ☐ A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
20. ☒ Other items or information:

Priority dates: 22 December 1998; 04 January 1999; and 28 January 1999.

U.S. APPLICATION NO. 09/868352 INTERNATIONAL APPLICATION NO. PCT/GB99/04377		ATTORNEY'S DOCKET NUMBER GJE-70	
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21. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$1000.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$710.00 International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$690.00 International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4) \$100.00 ENTER APPROPRIATE BASIC FEE AMOUNT =				CALCULATIONS PTO USE ONLY <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 50%;"></td> <td style="width: 50%;"></td> </tr> <tr> <td></td> <td style="text-align: right;">\$860.00</td> </tr> <tr> <td></td> <td style="text-align: right;">\$0.00</td> </tr> </table>					\$860.00		\$0.00
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Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).											
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE								
Total claims	19 - 20 =	0	x \$18.00								
Independent claims	9 - 3 =	6	x \$80.00								
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$270.00								
TOTAL OF ABOVE CALCULATIONS =			\$1,340.00								
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.			+ \$0.00								
SUBTOTAL =			\$1,340.00								
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).											
TOTAL NATIONAL FEE =			\$1,340.00								
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property			+ \$0.00								
TOTAL FEES ENCLOSED =			\$1,340.00								
			Amount to be refunded: \$								
			charged: \$								

a. ☐ A check in the amount of \$ _____ to cover the above fees is enclosed.

b. ☒ Please charge my Deposit Account No. 19-0065 in the amount of \$ 1,340.00 to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 19-0065. A duplicate copy of this sheet is enclosed.

d. ☐ Fees are to be charged to a credit card. **WARNING:** Information on this form may become public. **Credit card information should not be included on this form.** Provide credit card information and authorization on PTO-2038.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137 (a) or (b)) must be filed and granted to restore the application to pending status.

CORRESPONDENCE ADDRESS: _____

David Saliwanchik
SIGNATURE

CUSTOMER NUMBER **23,557**

June 15, 2001
DATE

David R. Saliwanchik
NAME

31,794
REGISTRATION NUMBER

June 15, 2001

09/868352
JC18 Rec'd PCT/PTO 1 5 JUN 2001
PRELIMINARY AMENDMENT
Patent Application

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Martin John Glenton Hughes, Joseph David Santangelo, Jonathan Douglas Lane, Robert Feldman, Joanne Christine Moore, Richard James Dobson, Paul Everest, Gordon Dougan, Rebecca Kerry Wilson

Docket No. : GJE-70

For : Genes and Proteins, And Their Use

Box PCT
Assistant Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Sir:

Please amend the above-identified patent application as follows:

In the Specification

After page 20: Please insert as new page 21 the attached Abstract of the Disclosure.

In the Claims

The following amendments are made with respect to the claims in the international application PCT/GB99/04377 attached as an Annex to the International Preliminary Examination Report (IPER). Therefore, please replace existing page 20 of the international application with the amended claim sheet (replacement page 20) of the annex attached to the IPER, and make the following amendments to the pending claims:

Please cancel claims 1-11 of claim sheet (replacement page 20) of the annex attached to the IPER and add the following new claims:

12. A peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

13. The peptide, according to claim 12, comprising an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

14. A polynucleotide wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29, obtainable from Group B *Streptococcus*; or said polynucleotide sequence comprises a homologue or a functional fragment of one said Group B *Streptococcus* genes.

15. A polynucleotide which encodes a peptide selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

16. A host transformed to express a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

17. The host, according to claim 16, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

18. A vaccine comprising either 1) a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes; or 2) a means for expressing said peptide.

19. The method, according to claim 18, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

20. A method for screening for potential drugs, wherein said method comprises the use of a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

21. The method, according to claim 20, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

22. A method for the detection of virulence, wherein said method comprises the use of a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

23. The method, according to claim 22, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

24. A method for the treatment or prevention of a condition associated with bacterial infection, wherein said method comprises administering to a patient in need of such treatment or prevention, an effective amount of a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

25. The method, according to claim 24, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

26. The method, according to claim 24, wherein the infection is a Group B *Streptococcal* infection.

27. The method, according to claim 24, wherein the infection is a local infection.

28. The method, according to claim 24, wherein the infection is a urinary tract infection.

29. An antibody raised against a peptide encoded by a polynucleotide sequence wherein said polynucleotide sequence comprises a gene, obtainable from a Group B *Streptococcus*, selected from the group consisting of pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29; or said polynucleotide sequence comprises a homologue or a functional fragment of one of said Group B *Streptococcus* genes.

30. The antibody, according to claim 29, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.

Remarks

Claims 1-11 have been canceled and new claims 12-30 have been added.

No new matter has been added by these amendments.

The Commissioner is hereby authorized to charge any fees under 37 CFR 1.16 or 1.17 as required by this paper to Deposit Account 19-0065.

Respectfully submitted,



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DRS/la

Attachment: Abstract of the Disclosure

GENES AND PROTEINS, AND THEIR USEField of the Invention

5 This invention relates to the identification of bacterial genes and proteins, and their use. More particularly, it relates to their use in therapy, for immunisation and in screening for drugs.

Background to the Invention

10 Group B *Streptococcus* (GBS), also known as *Streptococcus agalactiae*, is the causative agent of various conditions. In particular, GBS causes:
Early onset neonatal infection.

15 This infection usually begins in utero and causes severe septicaemia and pneumonia in infants, which is lethal if untreated and even with treatment is associated with a 10-20% mortality rate.

Late onset neonatal infection.

20 This infection occurs in the period shortly after birth until about 3 months of age. It causes a septicaemia, which is complicated by meningitis in 90% of cases. Other focal infections also occur including osteomyelitis, septic arthritis, abscesses and endophthalmitis.

Adult infections.

25 These appear to be increasingly common and occur most frequently in women who have just delivered a baby, the elderly and the immunocompromised. They are characterised by septicaemia and focal infections including osteomyelitis, septic arthritis, abscesses and
30 endophthalmitis.

Urinary tract infections.

GBS is a cause of urinary tract infections and in pregnancy accounts for about 10% of all infections.

Veterinary infections.

35 GBS causes chronic mastitis in cows. This, in turn, leads to reduced milk production and is therefore of considerable economic importance.

GBS infections can be treated with antibiotics. However, immunisation is preferable. It is therefore desirable to develop an immunogen that could be used in a therapeutically-effective vaccine.

5 Summary of the Invention

 The present invention is based on the identification of a series of genes in GBS, and also related organisms, the products of which may be localised on the outer surface of the organism and therefore may be used as a target for
10 immuno-therapy.

 According to one aspect of the invention, a peptide is encoded by an operon including any of the genes identified herein as pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50,
15 pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29, obtainable from Group B *Streptococcus*, or a homologue or functional fragment thereof. Such a peptide is suitable for therapeutic use, e.g. when isolated.

 The term "functional fragments" is used herein to
20 define a part of the gene or peptide which retains the activity of the whole gene or peptide. For example, a functional fragment of the peptide may be used as an antigenic determinant, useful in a vaccine or in the production of antibodies.

25 A gene fragment may be used to encode the active peptide. Alternatively, the gene fragment may have utility in gene therapy, targetting the wild-type gene *in vivo* to exert a therapeutic effect.

 A peptide according to the present invention may
30 comprise any of the amino acid sequences identified herein as SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35, or a functional fragment thereof.

 Because of the extracellular or cell surface location,
35 the peptides of the present invention may be suitable candidates for the production of therapeutically-effective vaccines against GBS. The term "therapeutically-effective"

is intended to include the prophylactic effect of vaccines. For example, a vaccine may comprise a peptide according to the invention, or the means for its expression, for the treatment of infection. The vaccine may be administered to females prior to or during pregnancy to protect mother and neonate against infection by GBS.

According to another aspect of the invention, the peptides or genes may be used for screening potential antimicrobial drugs or for the detection of virulence.

A further aspect of this invention is the use of any of the products identified herein, for the treatment or prevention of a condition associated with infection by a Group B Streptococcal strain.

Although the protein has been described for use in the treatment of patients, veterinary uses of the products of the invention are also considered to be within the scope of the present invention. In particular, the peptides or the vaccines may be used in the treatment of chronic mastitis, especially in cows.

Description of the Invention

The present invention is described with reference to Group B Streptococcal strain M732. However, all the GBS strains and many other bacterial strains are likely to include related peptides or proteins having amino acid sequence homology with the peptide of M732. Organisms likely to contain the peptides include, but are not limited to, *S. pneumoniae*, *S. pyogenes*, *S. suis*, *S. milleri*, Group C and Group G Streptococci and Enterococci. Vaccines to each of these may be developed in the same way as described for GBS.

Preferably, the peptides that may be useful for the production of vaccines have greater than 40% sequence similarity with the peptides identified herein. More preferably, the peptides have greater than 60% sequence similarity. Most preferably, the peptides have greater than 80% sequence similarity, e.g. 95% similarity.

Having characterised a gene according to the invention, it is possible to use the gene sequence to establish homologies in other microorganisms. In this way it is possible to determine whether other microorganisms have similar outer surface products. Sequence homologies may be established by searching in existing databases, e.g. EMBL or Genbank.

Peptides or proteins according to the invention may be purified and isolated by methods known in the art. In particular, having identified the gene sequence, it will be possible to use recombinant techniques to express the genes in a suitable host. Active fragments and homologues can be identified and may be useful in therapy. For example, the peptides or their active fragments may be used as antigenic determinants in a vaccine, to elicit an immune response. They may also be used in the preparation of antibodies, for passive immunisation, or diagnostic applications. Suitable antibodies include monoclonal antibodies, or fragments thereof, including single chain fv fragments. Methods for the preparation of antibodies will be apparent to those skilled in the art.

The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, e.g. alum, as necessary or desired, and used in therapy, to provide effective immunisation against Group B Streptococci or other related microorganisms. The preparation of vaccine formulations will be apparent to the skilled person.

More generally, and as is well known to those skilled in the art, a suitable amount of an active component of the invention can be selected, for therapeutic use, as can suitable carriers or excipients, and routes of administration. These factors will be chosen or determined according to known criteria such as the nature/severity of the condition to be treated, the type or health of the subject etc.

The products of the present invention were identified as follows:

A partial gene library of GBS (strain M732) chromosomal DNA was prepared using the plasmid vectors pFW-phoA1, pFW-phoA2 and pFW-phoA3 (Podbielski, A. et al. 1996. Gene 177:137-147). These plasmids possess a constitutive spectinomycin adenyltransferase antibiotic resistance marker, which confers a high level of spectinomycin resistance and is therefore easily selected. Furthermore, these vectors contain a truncated (leaderless) *Escherichia coli* *phoA* gene for alkaline phosphatase. The three vectors differ only with respect to the reading frame in which the leaderless *phoA* gene exists, as compared to an upstream in-frame *Bam*HI restriction enzyme site. Because this truncated *E. coli* *phoA* gene lacks the appropriate leader sequence for export of this enzyme across the bacterial membrane, extracellular alkaline phosphatase activity is absent when these plasmids are propagated in an *E. coli* *phoA* mutant (e.g. strain DH5 α). The chromogenic alkaline phosphatase substrate, XP (5-bromo-4-chloro-3-indolyl-phosphate), does not enter intact bacterial cells and therefore only exported or surface associated alkaline phosphatase activity can be detected. When exported or surface associated alkaline phosphatase activity is present, the chromogenic XP substrate is cleaved to yield a blue pigment and the corresponding bacterial colonies can be identified by their blue colour.

Plasmid DNA was digested to completion with *Bam*HI and dephosphorylated using shrimp alkaline phosphatase. GBS genomic DNA was partially digested with *Sau*3AI, size fractionated on a sucrose gradient and fragments <1kb in size were ligated into the prepared pFW-*phoA* vectors. *E. coli* strain DH5 α was chosen as the cloning host since it lacks a functional *phoA* gene. Recombinant plasmids were selected on Luria agar containing 100 μ g/ml of spectinomycin and 40 μ g/ml of the chromogenic XP substrate. *E. coli* transformants harbouring plasmids containing GBS

insert DNA that complements the export signal sequence of the leaderless *phoA* gene were identified by the blue colour of the colonies. Approximately 30000 different recombinant plasmids containing GBS insert DNA were screened in this manner and 83 recombinant plasmids, which complemented the leaderless *phoA*, were chosen for further study.

From these experiments, several clones were selected each containing a plasmid containing a gene (or part thereof), which complemented the leaderless *phoA*.

Having identified the gene in each clone it is then possible to obtain the full-length gene sequence, as follows.

Using the identified and sequenced gene fragment, oligonucleotide primers were designed for genomic DNA sequencing. These primers were designed so as to sequence in an 'outward' direction from the obtained sequence. Once read, the sequence obtained was checked to see if the 5' and 3' termini of the gene had been reached. The presence of these features was identified by checking against homologous sequences, and for the 5' end the presence of an AUG start codon (or accepted equivalent) preceded by a Shine-Dalgarno consensus sequence, and for the 3' end, the presence of a translation termination (Stop) codon.

Upon identification of the full-length gene, primers were designed for amplification of full-length product. Primers used included restriction enzyme recognition sites (NcoI at the 5' end and EcoO109I at the 3' end) to allow subsequent cloning of the product into the Lactococcal expression system used.

PCR was carried out using the primers, and the products cloned into a pCR 2.1 cloning vector (In Vitrogen). Following confirmation of the presence of the cloned fragment, the DNA was excised using the restriction enzymes NcoI and EcoO109I.

The vector into which this fragment was inserted was a modified version of pNZ8048 (Kuipers, O. P. et al. (1998) J. Biotech 64: 15-21). This vector, harbouring a

lactococcal origin of replication, a chloramphenicol resistance marker, an inducible nisin promoter and a multicloning site was altered by the replacement of the multicloning site with two 10X His tags, flanked on the 5-
5 most end with an NcoI site, split in the middle with a multicloning site (including an EcoO109I site), and a Stop (termination) codon at the 3'end of the His tags.

The gene of interest was inserted so that a 10X His tag was in the 3' position relative to the coding region.
10 Following transformation of the recombinant plasmid into *L.lactis* (strain NZ9000 - Kuipers, O. P. et al. (1998) *supra*), a 400 ml liquid culture was set up and translation of the protein was induced by the addition of nisin to the culture. After a 2 hour incubation, the cells were
15 harvested and lysed by bead beating. The resultant lysate was cleared by centrifugation, then passed over a metal affinity (Talon, Clonetech) column. The column was washed repeatedly before bound proteins were eluted with Imidazole.

20 To identify fractions containing the His-tagged recombinant protein, an aliquot from each fraction was analysed by SDS-PAGE, Western blotted and probed with anti-His antibodies.

The recombinant protein obtained was then used to
25 immunise New Zealand white rabbits, with pre-immune sera being harvested prior to immunisation. Following a boost, the rabbits were sacrificed and sera collected. This sera was used in Western blots, ELISA and animal protection models.

30 Using the sera obtained from the animal studies, immunosorption studies were carried out.

Group B *Streptococcus* was grown in 20ml Todd Hewitt broth (THB) for 8 hours, harvested and resuspended in 5ml PBS. 50µl aliquots of this were used to coat wells in a 96
35 well plate (Nunc Immuno-Sorb). This was left at 4°C overnight to allow for adsorbance of the bacteria onto the plate. Plates were washed twice with PBS, then blocked

with 3%BSA in PBS for 1hr at 37°C. Plates were again washed. Serial 10 fold dilutions of the sera were made in PBS and 50µl of these dilutions were added to the wells of the plate, in duplicate. The plate was covered and
5 incubated for 1 hr at 37°C. The plate was washed, then 50µl anti-rabbit alkaline phosphatase conjugated secondary antibody at a concentration of 1:5000 was added to each well. Following incubation at 37°C for an hour, the plate was washed again. 50µl substrate (PNPP) was added to each
10 well, and the reaction allowed to proceed for 30min before the adsorbance was read at 405 nm.

Animal protection studies were also carried out to test the effectiveness of protection on the immunised rabbits.

15 GBS M732 was grown up in THB until mid-log phase was reached - approximately 5 hours. Cells were counted in a counting chamber, and bacteria were diluted to give a concentration of 2×10^7 bacteria per ml in pre-immune or test sera. 50µl of this was injected via the
20 intraperitoneal route into 0-1 day old mice. The mice were observed for survival over 48 hours.

The following Examples illustrate the invention.

Example 1

25 A first clone contained a gene sequence identified herein as SEQ ID NO. 1, with an amino acid sequence identified as SEQ ID NO. 2, and classified as pho1-13.

A comparison of the amino acid sequence of pho1-13 was performed.

30 Homologues to the GBS pho1-13 gene product can be identified in *Streptococcus pyogenes*, *S. pneumoniae*, *S. salivarius*, *Escherichia coli*, *Yersinia enterocolitica*, *Aquifex aeolicus*, *Helicobacter pylori* and *Haemophilus influenzae*. The *S. pyogenes* and *S. pneumoniae* homologues
35 were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In all other cases, the above homologues

can be identified as ATP-dependent Clp protease proteolytic subunits. The catalytic activity of Clp proteases results in the hydrolysis of proteins to small peptides in the presence of ATP and magnesium (Giffard, P.M. et al. 1993. J. Gen. Microbiol. 139:913-920). Furthermore, the ClpP component of Clp proteases has been shown to be induced as part of the heat shock response (Kroh, H.E. and L.D. Simon. 1990. J. Bacteriol. 172:6026-6034) and it is probable that this subunit or the complete proteolytic domain would be associated with the bacterial surface.

Immunisation studies, carried out as described above, yielded the following results.

Treatment	No animals	No animals surviving	
		at time (hrs)	
		24	48
PBS	10	7	0
Pre-immunised	37	13	0
Immunised	38	17	9

Example 2

A second clone was selected containing a plasmid designated pho1-14. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences are shown as SEQ ID NOS. 3 and 4, respectively.

A comparison of the amino acid sequence of pho1-14 was performed.

Homologues to the GBS pho1-14 gene product can be identified in *Streptococcus pyogenes*, *Enterococcus faecalis* and *Streptococcus pneumoniae*. These homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. Additionally, two possible homologues were also

identified from *Shigella flexneri* (SpaR) and *Yersinia pseudotuberculosis* (YscT). These latter two homologues are related proteins, believed to be anchored in the bacterial membrane (Bergman, T. et al. 1994. J. Bacteriol. 176:2619-2626). In *S. flexneri*, the product of the *spaR* gene has been shown to be important for invasion of epithelial cells (Sasakawa, C. et al. 1993. J. Bacteriol. 175:2334-2346). Furthermore, the product of the *spaR* gene is also required for surface presentation of invasion plasmid antigens. The analogous protein in *Y. pseudotuberculosis* is a component of the Yop secretion system and is also important for virulence in this organism.

Example 3

A third clone was selected containing a plasmid designated pho1-5. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences are shown as SEQ ID NOS. 5 and 6.

A comparison of the amino acid sequence of pho1-5 was performed.

Homologues to the GBS pho1-5 gene product can only be identified in *Streptococcus pyogenes* and *Staphylococcus carnosus* (*sceA*). The *S. pyogenes* homologue was identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. Furthermore, little information is available on the function of the *sceA* gene product from *S. carnosus*. The *sceA* gene product shows some sequence similarity to the aggregation promoting protein from *Lactobacillus gasseri*. Based on analysis of the *sceA* gene product, this molecule contains a well-conserved signal sequence and is apparently secreted or associated with the bacterial cell surface.

Example 4

A further clone was selected containing a plasmid designated pho3-3. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The

nucleotide and deduced amino acid sequences are shown as SEQ ID NOS. 7 and 8.

A comparison of the amino acid sequence of pho3-3 was performed.

5 Homologues to the GBS pho3-3 gene product can be identified in *Streptococcus mutans* (rmlC), (cpsM) *S. pneumoniae* and *S. pyogenes*. The *S. pyogenes* homologue was identified from genome sequence data and no annotations were available as to the identity of the gene or gene
10 product. In *S. pneumoniae*, the homologue can be identified as dTDP-4-keto-6-deoxy glucose-3,5-epimerase. In the other two cases, the above homologues can be identified as dTDP-4-keto-L-rhamnose reductase (rmlC). In *S. mutans*, the gene encoding this enzyme, *rmlC*, is part of the *rml* locus.
15 The *rml* locus consists of three genes which exhibit significant similarity to enzymes involved in the biosynthesis of dTDP-rhamnose, the immediate precursor of the rhamnose component in the *S. mutans* polysaccharide capsule (Tsukioaka, Y. et al. 1997. J. Bacteriol. 179:1126-1134). An analogous locus has also been identified in *S. pneumoniae* (Coffey, T.J. et al. 1998. Mol. Microbiol. 17:73-83). Almost all *Streptococci* characteristically possess rhamnose in their cell wall associated polysaccharides (Schleifer, K.H. and R. Kilper-Bälz. 1987. Syst. Appl. Microbiol. 10:1-19), and it is highly probable that dTDP-4-keto-L-rhamnose reductase would be associated with the outer surface in *Streptococci*.

Example 5

A further clone was selected containing a plasmid designated pho2-10. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*.
30

The nucleotide sequence is shown as SEQ ID NO. 9. From this, upstream and downstream coding regions were identified, and the deduced amino acid sequences shown as
35 SEQ ID NOS. 10 and 11.

A comparison of the amino acid sequences of pho2-10 was performed.

Homologues to the GBS pho2-10 gene product can be identified in *Streptococcus pyogenes*, *Enterococcus faecalis*, *Debaryomyces occidentalis* (hatI) and *Escherichia coli* (trkD). The *S. pyogenes* and *E. faecalis* homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In the yeast *D. occidentalis*, the *hak1* gene is a homologue of the *trkD* gene from *E. coli* (Banuelos, M.A. et al. 1995. EMBO J. 14:3021-3027). The *trkD* gene of *E. coli* is part of the *kup* potassium uptake system. The specific homolog identified here is the *kup* system potassium uptake protein. The *kup* system is a constitutive potassium uptake system in *E. coli*. The *kup* system potassium uptake protein contains a highly hydrophobic N-terminus that is predicted to span the membrane at least 12 times. *Kup* is not homologous to other known membrane protein sequences. There is no indication of ATP binding, and it is proposed that the system is driven by a chemiosmotic gradient (Schleyer, M. & E.P. Bakker, 1993. J. Bacteriol. 175:6925-6931).

Example 6

A further clone was selected containing a plasmid designated pho2-15. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 12 and 13.

A comparison of the amino acid sequence of pho2-15 was performed.

Homologues to the GBS pho2-15 gene product can be identified in *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Enterococcus faecalis* and *Escherichia coli* (*gatC* and *SgcC*). The *S. pyogenes*, *S. pneumoniae* and *E. faecalis* homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In *E. coli*, the *gatC* and *sgcC* gene products can be identified as being the IIC component of phosphoenolpyruvate-dependent sugar

phosphotransferase systems (PTS), a major carbohydrate active-transport system. In PTS systems, the IIC component is typically involved in binding of extracellular carbohydrates and forms a complex with the IID component to constitute a membrane channel (Nobelmann, B. and J.W. Lengeler. 1995. Biochim. Biophys. Acta 1262:69-72).

Example 7

A further clone was selected containing a plasmid designated pho2-2. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 14 and 15, respectively.

A comparison of the amino acid sequence of pho2-2 was performed.

Homologues to the GBS pho2-2 gene product can be identified in *Enterococcus faecalis*, *Escherichia coli* (malK and afuC), *Bacillus subtilis* (glnO), *Haemophilus influenzae* (yebM and potA), *Streptococcus pyogenes*, *Streptococcus pneumoniae* and *Salmonella typhimurium* (malK). The *E. faecalis*, *S. pyogenes* and *S. pneumoniae* homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In all other cases, homologues represented ATP-binding transport proteins that are part of ABC type transporters. Many of the components of ABC type transporters are membrane or cell surface associated, as these systems are involved in the transport of macromolecules from the extracellular environment to the intracellular compartment.

Example 8

A further clone was selected containing a plasmid designated pho3-14. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 16 and 17.

A comparison of the amino acid sequence of pho3-14 was performed and no homologues could be identified in any of

the public databases. One homologue to the GBS pho3-14 gene product can be identified in *Streptococcus pyogenes*, but this homologue was identified from genome sequence data and no annotations were available as to the identity of the gene or gene product. Using this *S. pyogenes* homologue to search the public databases yielded no further information. Since the pho3-14 product complemented the leaderless *phoA* gene, it can be concluded that this protein (or part thereof) would most probably be located extracellularly.

10 Example 9

A further clone was selected containing a plasmid designated pho3-17. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 18 and 19.

A comparison of the amino acid sequence of pho3-17 was performed.

Homologues to the GBS Pho3-17 gene product can be identified in *Streptococcus mutans* and *Lactococcus lactis*, with similarity being shown to N-acetyl muramidase. Similarity is also seen with an unidentified gene, yubE from *Bacillus subtilis*.

N-acetylmuramidase is an autolysin that is involved in cell division. Using this limited information along with the fact that pho3-17 complemented the leaderless *phoA* gene, it can be concluded that the pho3-17 product would most probably be located extracellularly.

Example 10

A further clone was selected containing a plasmid designated pho3-18. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 20 and 21.

A comparison of the amino acid sequence of pho3-18 was performed.

Homologues to the GBS pho3-18 gene product can be identified in *Streptococcus pyogenes* and *Streptococcus*

pneumoniae. These homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. Using these *S. pyogenes* and *S. pneumoniae* homologues to search the public databases showed some similarity to outer surface and membrane spanning proteins. Since the ORF3-18 product complemented the leaderless *phoA* gene, it can be concluded that this protein (or part thereof) would most probably be located extracellularly.

10 Example 11

A further clone was selected containing a plasmid designated pho3-1. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 22 and 23.

A comparison of the amino acid sequence of pho3-1 was performed.

Homologues to the GBS pho3-1 gene product can be identified in *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Bacillus subtilis* (*yutD*) and *Enterococcus faecalis*. The *S. pyogenes*, *S. pneumoniae* and *E. faecalis* homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In *B. subtilis*, the function of the *yutD* gene product is unknown. It can be noted however, that the *yutD* gene is located on the *B. subtilis* chromosome in a region containing genes involved in cell wall synthesis. The fact that this DNA sequence complemented the leaderless *phoA* gene suggests that this gene product is extracellularly located.

30 Example 12

A further clone was selected containing a plasmid designated pho3-21. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 24 and 25.

A comparison of the amino acid sequence of pho3-21 was performed.

Homologues to the GBS pho3-21 gene product can be identified in *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Lactobacillus fermentum* (bspA) and *Lactobacillus reuteri* (cnb). The *S. pyogenes* and *S. pneumoniae* homologues were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In *L. fermentum*, the bspA gene product has been identified as being a basic cell surface-located protein that has some sequence similarity to family III of the bacterial solute-binding proteins (Turner, M.S. et al. 1997. J. Bacteriol. 179:3310-3316). In *L. reuteri*, the cnb gene product has been identified as a collagen binding protein that has some sequence similarity to the solute-binding component of bacterial ABC transporters (Roos, S. et al. 1996. FEMS Microbiol. Lett. 144:33-38).

Example 13

A further clone was selected containing a plasmid designated pho3-22. This plasmid contained a gene (or part thereof), which complemented the leaderless phoA. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 26 and 27.

A comparison of the amino acid sequence of pho3-22 was performed.

Homologues to the GBS pho3-22 gene product can be identified in *Enterococcus faecalis*, *Streptococcus equisimilis* (lppC), *Pseudomonas fluorescens* (oprI) and *Streptococcus thermophilus* (orf142). The *E. faecalis* homolog was identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In *S. equisimilis*, the lppC gene product has been identified as being a lipoprotein that is homologous to the E(P4) outer membrane protein from *Haemophilus influenzae* (Gase, K. et al. 1997. Med. Microbiol. Immunol. 186:63-73). Likewise, the P.

fluorescens *oprI* gene encodes a major outer membrane lipoprotein (Cornelis, P. et al. 1989. Mol. Microbiol. 3:421-428). In *S. thermophilus*, the *orf142* product has been putatively identified as a cell surface exposed
5 lipoprotein that may act as a receptor for the bacteriophages TP-J34 and Sfi21 (Neve, H. et al. 1998. Virology 241:61-72). The ORF3-22 product showed good similarity to the above homologues, particularly at the N-terminus. This is most likely the region required for
10 complementation of the leaderless *phoA* gene, and therefore serves as a leader sequence.

Example 14

A further clone was selected containing a plasmid designated *pho3-23*. This plasmid contained a gene (or part
15 thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the genes are shown as SEQ ID NOS. 28 and 29.

A comparison of the amino acid sequence of *pho3-23* was performed.

20 Homologues to the GBS *pho3-23* gene product can be identified in *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Enterococcus faecalis* and *Streptococcus mutans* (*perM*). The *S. pyogenes*, *S. pneumoniae* and *E. faecalis* homologues were identified from genome sequence data and no
25 annotations were available as to the identity of the gene or gene products. In *S. mutans*, the *perM* gene product has been presumptively identified as a permease, but no other information is available as to the function of this protein. Considering that the *pho3-23* coding region
30 complements the leaderless *phoA* gene, it can be concluded that the *pho3-17* gene product would most probably be located extracellularly.

Example 15

A further clone was selected containing a plasmid designated *pho3-24*. This plasmid contained a gene (or part
35 thereof), which complemented the leaderless *phoA*. The

nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 30 and 31.

A comparison of the amino acid sequence of pho3-24 was performed.

- 5 Homologues to the GBS pho3-24 gene product can be identified in *Streptococcus mutans* (dltB), *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Enterococcus faecalis*, *Lactobacillus casei* (dltB) and *Bacillus subtilis* (dltB). The *S. pneumoniae*, *S. pyogenes* and *E. faecalis* homologues
- 10 were identified from genome sequence data and no annotations were available as to the identity of the gene or gene products. In *S. mutans*, *L. casei* and *B. subtilis*, the dltB gene product has been identified as being a basic membrane protein that is involved in the transport of
- 15 activated D-alanine through the cell membrane. The dltB gene product is involved in the biosynthesis of D-alanyl-lipoteichoic acid (Heaton, M.P. and F.C. Neuhaus. 1992. J. Bacteriol. 174:4707-4717). In *L. casei* and *B. subtilis*, the dltB gene product is believed to contain at least 9
- 20 membrane spanning domains, indicating that the protein or portions thereof are exposed to the outside of the cell.

Example 16

A further clone was selected containing a plasmid designated pho3-29. This plasmid contained a gene (or part thereof), which complemented the leaderless phoA. The

25 nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 32 and 33.

A comparison of the amino acid sequence of pho3-29 was performed.

- 30 Homologues to the GBS pho3-29 gene product can be identified in *Borrelia burgdorferi* (p23 or ospC), *Bacillus brevis* (owp) and *Pseudomonas aeruginosa* (oprI). Although these homologues are not related to each other, they all represent major outer surface proteins. In *B. burgdorferi*,
- 35 the ospC gene product has been identified as being a 23-kDa protein that is the immunodominant antigen on the surface of this bacterium (Padula, S.J. et al. 1993. Infect. Immun.

- 61:5097-5105). The *owp* gene product from *B. brevis* is one of two major cell wall proteins involved in the surface layer lattice (Tsuboi, A. 1988. J. Bacteriol. 170:935-945). Finally, the *oprI* gene from *P. aeruginosa* encodes a major outer membrane lipoprotein precursor (Saint-Onge, A. et al. 1992. J. Gen. Microbiol. 138:733-741).

Example 17

- A further clone was selected containing a plasmid designated pho3-50. This plasmid contained a gene (or part thereof), which complemented the leaderless *phoA*. The nucleotide and deduced amino acid sequences of the gene are shown as SEQ ID NOS. 34 and 35.

A comparison of the amino acid sequence of pho3-50 was performed.

- Homologues to the GBS pho3-50 gene product can be identified in a variety of Streptococci (*penA*, *pbp2B*, *pbpB2*), *Borrelia burgdorferi* (*pbp2*), *Enterococcus faecalis* (*pbpC*), *Staphylococcus aureus* (*pbpA*), *Mycobacterium leprae* (*pbpB*) and *Helicobacter pylori* (*pbp2*). In all cases, the above homologues can be identified as penicillin binding proteins (PBPs). Genes encoding penicillin binding proteins are often located in a cluster of genes associated with cell wall synthesis (Pucci, M.J. et al. 1997. J. Bacteriol. 179:5632-5635). Furthermore, PBPs are typically integrated into the cell wall of a bacterium with some or all of the protein being exposed on the outer bacterial surface.

CLAIMS

1. A peptide encoded by an operon including any of the genes identified herein as pho1-13, pho3-21, pho2-15, pho3-18, pho3-22, pho3-3, pho3-17, pho2-2, pho1-5, pho3-1, pho3-23, pho3-50, pho1-14, pho2-10, pho3-14, pho3-24 and pho3-29, obtainable from Group B *Streptococcus*, or a homologue thereof or a functional fragment thereof, for therapeutic use.
2. A peptide according to claim 1, comprising any of the amino acid sequences identified herein as SEQ ID NOS. 2, 4, 6, 8, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33 and 35.
3. A polynucleotide encoding a peptide according to claim 1 or claim 2, for therapeutic use.
4. A host transformed to express a peptide according to claim 1 or claim 2.
5. A vaccine comprising a peptide according to claim 1 or claim 2, or the means for its expression.
6. Use of a product according to any of claims 1 to 4, for screening potential drugs or for the detection of virulence.
7. Use of a product according to any of claims 1 to 4, for the manufacture of a medicament for use in the treatment or prevention of a condition associated with bacterial infection.
8. Use according to claim 7, wherein the infection is a Group B streptococcal infection.
9. Use according to claim 7 or claim 8, wherein the infection is a focal infection.
10. Use according to claim 7 or claim 8, wherein the infection is a urinary tract infection.
11. An antibody raised against a peptide according to claim 1 or claim 2.

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35

40

45

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Ser Lys Ala Asp Lys Val Arg Val Ala Lys Lys Ser Lys Met Thr Lys
 50 55 60

Ala Thr Ser Lys Ser Lys Val Glu Asp Val Lys Gln Ala Pro Lys Pro
 65 70 75 80

Ser Gln Ala Ser Asn Glu Ala Pro Lys Ser Ser Ser Gln Ser Thr Glu
 85 90 95

Ala Asn Ser Gln Gln Gln Val Thr Ala Ser Glu Glu Thr Ala Val Glu
 100 105 110

Gln Ala Val Val Thr Glu Ile Pro Leu Leu Pro Val Arg His Asn Asn
 115 120 125

Leu Tyr Ala Val Thr Glu Thr Pro Tyr Asn Pro Ala Gln Pro Pro Asp
 130 135 140

Gln Val Ala Arg Tyr Glu Gln Trp Lys Tyr Cys Gln Ala Val Gly Ser
 145 150 155 160

Ala Ala Ala Ala Gln Met Ala Ala Ala Thr Gly Val Pro Gln Ser Thr
 165 170 175

Trp Glu His Ile Ile Ala Arg Glu Ser Asn Gly Asn Pro Asn Val Ala
 180 185 190

Asn Ala Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly
 195 200 205

Ser Thr Ala Thr Val Gln Asp Gln Val Ile Gln Leu Leu Lys Leu Ile
 210 215 220

Arg Ala Gln Gly Leu Ser Ala Gly Tyr Gln
 225 230

<210> 7

<211> 594

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(594)

<400> 7

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 1 5 10 15

gcc att cct gaa ttg ttg gaa ttc gat att acc gtt cgt gga gac aac 96
 Ala Ile Pro Glu Leu Leu Glu Phe Asp Ile Thr Val Arg Gly Asp Asn
 20 25 30

cgt gga tgg ttc aaa gag aac ttt caa aaa gaa aaa atg ata ccg ctt 144
 Arg Gly Trp Phe Lys Glu Asn Phe Gln Lys Glu Lys Met Ile Pro Leu
 35 40 45

ggc ttc cca gaa agc ttc ttt gag gca gac aaa cta caa aat aat att 192
 Gly Phe Pro Glu Ser Phe Phe Glu Ala Asp Lys Leu Gln Asn Asn Ile
 50 55 60

tcg ttt aca aaa aaa aat act ttg cga ggt ctc cat gca gag cct tgg 240
 Ser Phe Thr Lys Lys Asn Thr Leu Arg Gly Leu His Ala Glu Pro Trp
 65 70 75 80

gat aaa tat gtt tcg atc gct gat gaa gga cgt gtg atc ggt act tgg 288
 Asp Lys Tyr Val Ser Ile Ala Asp Glu Gly Arg Val Ile Gly Thr Trp
 85 90 95

gtt gac ctc cgt gaa ggt gac agt ttt ggt aac gtt tac caa acg att 336
 Val Asp Leu Arg Glu Gly Asp Ser Phe Gly Asn Val Tyr Gln Thr Ile
 100 105 110

atc gat gcc tca aaa ggt att ttt gtt cca cgc ggc gtt gct aat ggt 384
 Ile Asp Ala Ser Lys Gly Ile Phe Val Pro Arg Gly Val Ala Asn Gly
 115 120 125

ttc caa gtt ctt tca gat aaa gca gct tat act tat ctc gtt aac gat 432
 Phe Gln Val Leu Ser Asp Lys Ala Ala Tyr Thr Tyr Leu Val Asn Asp
 130 135 140

tat tgg gca ctt gaa ctc aaa cca aaa tat gct ttc gtt aac tat gca 480
 Tyr Trp Ala Leu Glu Leu Lys Pro Lys Tyr Ala Phe Val Asn Tyr Ala
 145 150 155 160

gat cca aat cta ggc att cag tgg gaa aat ctw gaa gaa gca gaa gtc 528
 Asp Pro Asn Leu Gly Ile Gln Trp Glu Asn Xaa Glu Glu Ala Glu Val
 165 170 175

tca gaa gca gat aag aat cac cca ctt ctc aaa gat gta aaa cct ttg 576
 Ser Glu Ala Asp Lys Asn His Pro Leu Leu Lys Asp Val Lys Pro Leu
 180 185 190

aag aag gaa gat ttg taa 594
 Lys Lys Glu Asp Leu
 195

<210> 8

<211> 197

<212> PRT

<213> group B streptococcus

<400> 8

Met Thr Glu Pro Phe Phe Asp Lys Glu Leu Thr Cys Arg Pro Ile Glu
 1 5 10 15

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 20 25 30

Arg Gly Trp Phe Lys Glu Asn Phe Gln Lys Glu Lys Met Ile Pro Leu
 35 40 45

Gly Phe Pro Glu Ser Phe Phe Glu Ala Asp Lys Leu Gln Asn Asn Ile
 50 55 60

Ser Phe Thr Lys Lys Asn Thr Leu Arg Gly Leu His Ala Glu Pro Trp

65	70	75	80
Asp Lys Tyr Val Ser Ile Ala Asp Glu Gly Arg Val Ile Gly Thr Trp	85	90	95
Val Asp Leu Arg Glu Gly Asp Ser Phe Gly Asn Val Tyr Gln Thr Ile	100	105	110
Ile Asp Ala Ser Lys Gly Ile Phe Val Pro Arg Gly Val Ala Asn Gly	115	120	125
Phe Gln Val Leu Ser Asp Lys Ala Ala Tyr Thr Tyr Leu Val Asn Asp	130	135	140
Tyr Trp Ala Leu Glu Leu Lys Pro Lys Tyr Ala Phe Val Asn Tyr Ala	145	150	155
Asp Pro Asn Leu Gly Ile Gln Trp Glu Asn Xaa Glu Glu Ala Glu Val	165	170	175
Ser Glu Ala Asp Lys Asn His Pro Leu Leu Lys Asp Val Lys Pro Leu	180	185	190
Lys Lys Glu Asp Leu	195		

<210> 9
 <211> 1217
 <212> DNA
 <213> group B streptococcus

<220>
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 <222> (1)..(570)

<220>
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 <222> (679)..(945)

<400> 9	
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Tyr Tyr Leu Ile Gly Gly Leu Ala Glu Met Gln His Val Asn His Ser	
1 5 10 15	
tct ttt gat aaa gca tca aaa gca gga ttt att att gct tta ggc att	96
Ser Phe Asp Lys Ala Ser Lys Ala Gly Phe Ile Ile Ala Leu Gly Ile	

	20	25	30	
gtt tat gga gat att ggt aca agc cca ctc tat acg atg caa tca ttg				144
Val Tyr Gly Asp Ile Gly Thr Ser Pro Leu Tyr Thr Met Gln Ser Leu				
	35	40	45	
gtt gaa aac caa ggt ggt att tct agt gtc aca gaa tcg ttt atc tta				192
Val Glu Asn Gln Gly Gly Ile Ser Ser Val Thr Glu Ser Phe Ile Leu				
	50	55	60	
ggt tct ata tct tta atc ata tgg acc ttg aca ctt att aca act atc				240
Gly Ser Ile Ser Leu Ile Ile Trp Thr Leu Thr Leu Ile Thr Thr Ile				
	65	70	75 80	
aag tat gtg ctt gta gct tta aag gcg gat aat cac cac gaa ggt ggt				288
Lys Tyr Val Leu Val Ala Leu Lys Ala Asp Asn His His Glu Gly Gly				
	85	90	95	
att ttt tct tta tat acc ctt gtt aga aaa atg aca cct tgg tta att				336
Ile Phe Ser Leu Tyr Thr Leu Val Arg Lys Met Thr Pro Trp Leu Ile				
	100	105	110	
gtt ccg gct gtt att gga ggt gca acc ttg ttg tca gat gga gct ttg				384
Val Pro Ala Val Ile Gly Gly Ala Thr Leu Leu Ser Asp Gly Ala Leu				
	115	120	125	
acg cca gct gta acc gta ctt cag ccg tta agg att aaa gta gtt cct				432
Thr Pro Ala Val Thr Val Leu Gln Pro Leu Arg Ile Lys Val Val Pro				
	130	135	140	
agt ttg cag cat att tcc aga atc aga gta tgt tat ttt gcg acc ttg				480
Ser Leu Gln His Ile Ser Arg Ile Arg Val Cys Tyr Phe Ala Thr Leu				
	145	150	155 160	
tta ttt act gtt act ttt gcc atc caa ggt ttg gaa cgg gtg tta ttg				528
Leu Phe Thr Val Thr Phe Ala Ile Gln Gly Leu Glu Arg Val Leu Leu				
	165	170	175	
gaa tta ttg gcc att atg tta tat ggt ttg cct ttt ggt tta				570
Glu Leu Leu Ala Ile Met Leu Tyr Gly Leu Pro Phe Gly Leu				
	180	185	190	
ncgggtctcct tatagttttg cccatccaga agttttcaag cattaatcca tactacggtt				630
tgaaattgtt atttagtcca gagaatcata aaggtatttt tatttttag gat cta ttt				687
			Asp Leu Phe	
tcc tgg cga caa acg gga gca gaa gca cta tac tct gac tta ggt cat				735

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Ser Trp Arg Gln Thr Gly Ala Glu Ala Leu Tyr Ser Asp Leu Gly His
195                200                205

ggt ggg cgt gga aat ata cat gtt tca tgg ccg ttc gtt aag gtt gcc 783
Val Gly Arg Gly Asn Ile His Val Ser Trp Pro Phe Val Lys Val Ala
210                215                220                225

att ata ctt tct tat tgt ggg caa ggg gca tgg att tta gct aat aag 831
Ile Ile Leu Ser Tyr Cys Gly Gln Gly Ala Thr Ile Leu Ala Asn Lys
                230                235                240

aac gca gga aat gaa ttg aat ccc ttt ttt gct agt att cct tcg caa 879
Asn Ala Gly Asn Glu Leu Asn Pro Phe Phe Ala Ser Ile Pro Ser Gln
                245                250                255

ttt aca atg cat gtc gtt att tta gct act ttg gca gct atc atc gct 927
Phe Thr Met His Val Val Ile Leu Ala Thr Leu Ala Ala Ile Ile Ala
                260                265                270

tca cag gca ctg att tct ggatcaattt accttaagtt ctgagctatg          975
Ser Gln Ala Leu Ile Ser
275

cgactaaaaa tattccacata atttcgttca acttatcctg ttgacaatat tgggtcaaac 1035

ctacatacct ggtattaatt ggttcttatt tgccattaca acctctattg gtttgetttt 1095

taagacttca gcgcacatgg aagcagcata tggattagcg ataacaatta cgatgctaata 1155

gacaactatt ttactgtctt tctttttaat tcaaaaagga gtaaagagag gttttagcta 1215

tt                                                                    1217

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<210> 10

<211> 190

<212> PRT

<213> group B streptococcus

<400> 10

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Tyr Tyr Leu Ile Gly Gly Leu Ala Glu Met Gln His Val Asn His Ser
1                5                10                15

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Ser Phe Asp Lys Ala Ser Lys Ala Gly Phe Ile Ile Ala Leu Gly Ile
20                25                30

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Val Tyr Gly Asp Ile Gly Thr Ser Pro Leu Tyr Thr Met Gln Ser Leu
35                40                45

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Val Glu Asn Gln Gly Gly Ile Ser Ser Val Thr Glu Ser Phe Ile Leu
50 55 60

Gly Ser Ile Ser Leu Ile Ile Trp Thr Leu Thr Leu Ile Thr Thr Ile
65 70 75 80

Lys Tyr Val Leu Val Ala Leu Lys Ala Asp Asn His His Glu Gly Gly
85 90 95

Ile Phe Ser Leu Tyr Thr Leu Val Arg Lys Met Thr Pro Trp Leu Ile
100 105 110

Val Pro Ala Val Ile Gly Gly Ala Thr Leu Leu Ser Asp Gly Ala Leu
115 120 125

Thr Pro Ala Val Thr Val Leu Gln Pro Leu Arg Ile Lys Val Val Pro
130 135 140

Ser Leu Gln His Ile Ser Arg Ile Arg Val Cys Tyr Phe Ala Thr Leu
145 150 155 160

Leu Phe Thr Val Thr Phe Ala Ile Gln Gly Leu Glu Arg Val Leu Leu
165 170 175

Glu Leu Leu Ala Ile Met Leu Tyr Gly Leu Pro Phe Gly Leu
180 185 190

<210> 11

<211> 89

<212> PRT

<213> group B streptococcus

<400> 11

Asp Leu Phe Ser Trp Arg Gln Thr Gly Ala Glu Ala Leu Tyr Ser Asp
1 5 10 15

Leu Gly His Val Gly Arg Gly Asn Ile His Val Ser Trp Pro Phe Val
20 25 30

Lys Val Ala Ile Ile Leu Ser Tyr Cys Gly Gln Gly Ala Trp Ile Leu
35 40 45

Ala Asn Lys Asn Ala Gly Asn Glu Leu Asn Pro Phe Phe Ala Ser Ile
50 55 60

Pro Ser Gln Phe Thr Met His Val Val Ile Leu Ala Thr Leu Ala Ala

<210> 13

<211> 125

<212> PRT

<213> group B streptococcus

<400> 13

Met Gln Val Phe Leu Asn Ile Val Asn Lys Phe Phe Asp Pro Val Ile
 1 5 10 15

His Met Gly Ser Gly Val Val Met Leu Ile Val Met Thr Gly Leu Ala
 20 25 30

Met Ile Phe Gly Val Lys Phe Ser Lys Ala Leu Glu Gly Gly Ile Lys
 35 40 45

Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu Thr
 50 55 60

Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly Ile
 65 70 75 80

Asn Leu Ser Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile Thr
 85 90 95

Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Ile Met Leu Ile Val
 100 105 110

Asn Ile Val Met Ile Val Met Lys Lys Lys Arg Ile Pro
 115 120 125

<210> 14

<211> 705

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (118)..(705)

<400> 14

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acatattgcc aaagttttga tattattact ataatatagt ttgtagagga gaataat 117

atg ggc caa gaa cct atc atc gaa tat caa aat atc aat aaa gtg tat	165
Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr	
1 5 10 15	
ggg gaa aat gtt gcg gtt gaa gat att aac ctt aaa att tac cct ggt	213
Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly	
20 25 30	
gat ttc gtt tgt ttc atc ggt acg agt gga tca ggt aaa aca aca tta	261
Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu	
35 40 45	
atg cgt atg gtt aac cat atg tta aaa cca aca aat ggt act cta tta	309
Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu	
50 55 60	
ttt aag gga aaa gat atc tct act att aac ccc att gaa tta aga cgc	357
Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg	
65 70 75 80	
aga att gga tat gtt atc caa aac att ggt tta atg cct cat atg acc	405
Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr	
85 90 95	
att tac gaa aat ata gtt ctt gta cca aaa tta ttg aaa tgg tca gaa	453
Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu	
100 105 110	
gaa gct aaa aga gct aaa gca agg gaa ctt att aaa tta gtt gaa tta	501
Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu	
115 120 125	
ccc gaa gaa tat ttg gat cgc tac cct agt gag ttg tct ggc ggt cag	549
Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln	
130 135 140	
caa caa cgt atc ggt gtc att cgc gct ctt gca gca gac caa gat att	597
Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile	
145 150 155 160	
att tta atg gat gag cct ttt gga gct ctg gat cct att act aga gaa	645
Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu	
165 170 175	
ggt att caa gac ttt agt caa gtc tct tca gga aga aat ggg gga aaa	693
Gly Ile Gln Asp Phe Ser Gln Val Ser Ser Gly Arg Asn Gly Gly Lys	
180 185 190	

cta tca tct tag
 Leu Ser Ser
 195

705

<210> 15
 <211> 195
 <212> PRT
 <213> group B streptococcus

<400> 15

Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr
 1 5 10 15

Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly
 20 25 30

Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
 35 40 45

Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
 50 55 60

Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
 65 70 75 80

Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr
 85 90 95

Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu
 100 105 110

Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu
 115 120 125

Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln
 130 135 140

Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile
 145 150 155 160

Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu
 165 170 175

Gly Ile Gln Asp Phe Ser Gln Val Ser Ser Gly Arg Asn Gly Gly Lys
 180 185 190

Leu Ser Ser

195

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 <211> 367
 <212> DNA
 <213> group B streptococcus

<220>
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 <222> (1)..(366)

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 ile pro tyr ser asp val phe ala thr gly gly phe leu tyr tyr val
 1 5 10 15
 acg att gct cta agt tac ctt tta ggg tct agt atc tgg tta ttt att 96
 thr ile ala leu ser tyr leu leu gly ser ser ile trp leu phe ile
 20 25 30
 gta cag ttt att gct tac tat gta tct gga att tat ttt tat aaa tta 144
 val gln phe ile ala tyr tyr val ser gly ile tyr phe tyr lys leu
 35 40 45
 gtt tat tat gtg gca caa agt gaa att gtc tcg ata ggc atg acg ttg 192
 val tyr tyr val ala gln ser glu ile val ser ile gly met thr leu
 50 55 60
 att ttc tat ata atg aat att gtc tta gga ttc ggt ggt atg tac cca 240
 ile phe tyr ile met asn ile val leu gly phe gly gly met tyr pro
 65 70 75 80
 ata cag tgg gca tta cct ttt atg ctc att tcg cta tgg ttt tta att 288
 ile gln trp ala leu pro phe met leu ile ser leu trp phe leu ile
 85 90 95
 aaa ttt tgt gtc gat aat atc gtt gat gaa gca ttt ata ttt tat ggt 336
 lys phe cys val asp asn ile val asp glu ala phe ile phe tyr gly
 100 105 110
 att tta gca gca ttc tca cta ttt ata gat c 367
 ile leu ala ala phe ser leu phe ile asp
 115 120

<210> 17

<211> 122

<212> PRT

<213> group B streptococcus

<400> 17

Ile Pro Tyr Ser Asp Val Phe Ala Thr Gly Gly Phe Leu Tyr Tyr Val
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Thr Ile Ala Leu Ser Tyr Leu Leu Gly Ser Ser Ile Trp Leu Phe Ile
 20 25 30

Val Gln Phe Ile Ala Tyr Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu
 35 40 45

Val Tyr Tyr Val Ala Gln Ser Glu Ile Val Ser Ile Gly Met Thr Leu
 50 55 60

Ile Phe Tyr Ile Met Asn Ile Val Leu Gly Phe Gly Gly Met Tyr Pro
 65 70 75 80

Ile Gln Trp Ala Leu Pro Phe Met Leu Ile Ser Leu Trp Phe Leu Ile
 85 90 95

Lys Phe Cys Val Asp Asn Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly
 100 105 110

Ile Leu Ala Ala Phe Ser Leu Phe Ile Asp
 115 120

<210> 18

<211> 570

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(570)

<400> 18

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 Met Arg Lys Arg Phe Ser Leu Leu Asn Phe Ile Val Val Thr Phe Ile
 1 5 10 15

ttc ttt ttc ttt att ctt ttt ccg ctt tta aac cat aag gga aaa gta 96
 Phe Phe Phe Phe Ile Leu Phe Pro Leu Leu Asn His Lys Gly Lys Val
 20 25 30

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gat gct aat tct agg cag agt gtt acc tac acc aaa gaa gaa ttt ata 144
Asp Ala Asn Ser Arg Gln Ser Val Thr Tyr Thr Lys Glu Glu Phe Ile
      35                      40                      45

caa aaa att gtg cca gat gcg caa gat cta gga aag tcg tac ggt att 192
Gln Lys Ile Val Pro Asp Ala Gln Asp Leu Gly Lys Ser Tyr Gly Ile
      50                      55                      60

cgt cct tca ttt att att gca cag gcg gct ttg gat tct gat ttc gga 240
Arg Pro Ser Phe Ile Ile Ala Gln Ala Ala Leu Asp Ser Asp Phe Gly
      65                      70                      75                      80

gag aaa tat agc tat agt atc ata atc tgt tgg ttg ctt gca gaa cca 288
Glu Lys Tyr Ser Tyr Ser Ile Ile Ile Cys Trp Leu Leu Ala Glu Pro
      85                      90                      95

gga acg ccc tca att acc tta aat gat agt agt aca gga aaa aaa cag 336
Gly Thr Pro Ser Ile Thr Leu Asn Asp Ser Ser Thr Gly Lys Lys Gln
      100                      105                      110

gaa aag caa ttt act cat tat aaa tct tgg aag tat tca atg gat gat 384
Glu Lys Gln Phe Thr His Tyr Lys Ser Trp Lys Tyr Ser Met Asp Asp
      115                      120                      125

tac ctt gct cat ata aaa tct gga gcg aca ggc aaa aaa gat tca tat 432
Tyr Leu Ala His Ile Lys Ser Gly Ala Thr Gly Lys Lys Asp Ser Tyr
      130                      135                      140

act ata atg gtg tct gtt aaa aat cca aaa act tta gtg caa aaa tta 480
Thr Ile Met Val Ser Val Lys Asn Pro Lys Thr Leu Val Gln Lys Leu
      145                      150                      155                      160

caa gat agt ggt ttt gat aat gac aaa aag tac gct aaa aaa atg acg 528
Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
      165                      170                      175

gaa atc att gat ttg tat gat tta aca aga tat gat aag tga 570
Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
      180                      185                      190

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<210> 19

<211> 189

<212> PRT

<213> group B streptococcus

<400> 19

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Met Arg Lys Arg Phe Ser Leu Leu Asn Phe Ile Val Val Thr Phe Ile
 1             5             10             15

Phe Phe Phe Phe Ile Leu Phe Pro Leu Leu Asn His Lys Gly Lys Val
          20             25             30

Asp Ala Asn Ser Arg Gln Ser Val Thr Tyr Thr Lys Glu Glu Phe Ile
          35             40             45

Gln Lys Ile Val Pro Asp Ala Gln Asp Leu Gly Lys Ser Tyr Gly Ile
          50             55             60

Arg Pro Ser Phe Ile Ile Ala Gln Ala Ala Leu Asp Ser Asp Phe Gly
          65             70             75             80

Glu Lys Tyr Ser Tyr Ser Ile Ile Ile Cys Trp Leu Leu Ala Glu Pro
          85             90             95

Gly Thr Pro Ser Ile Thr Leu Asn Asp Ser Ser Thr Gly Lys Lys Gln
          100            105            110

Glu Lys Gln Phe Thr His Tyr Lys Ser Trp Lys Tyr Ser Met Asp Asp
          115            120            125

Tyr Leu Ala His Ile Lys Ser Gly Ala Thr Gly Lys Lys Asp Ser Tyr
          130            135            140

Thr Ile Met Val Ser Val Lys Asn Pro Lys Thr Leu Val Gln Lys Leu
          145            150            155            160

Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
          165            170            175

Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
          180            185

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<210> 20

<211> 978

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(978)

<400> 20

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1 5 10 15	
ata att tct tac cca aaa atg acg gaa tta aca aag tcc gtt gaa aaa	96
Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys	
20 25 30	
caa ctt gaa gat aat gct gat aat cta tca gac caa ctg aca tat cag	144
Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln	
35 40 45	
ata gaa gtg gcg caa aaa gat caa atc tac gtg act aat cag cta aac	192
Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn	
50 55 60	
cgt atg caa cag gaa att atc agt cgc tta ccg ata tgc gta cag aat	240
Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn	
65 70 75 80	
aaa tca gca tta acg gag agt cga gat cga tca gac aaa cgc ttg gaa	288
Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu	
85 90 95	
ttg att aac tcc aat tta tct cag tca gtt cag aaa atg caa gat tca	336
Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser	
100 105 110	
atg aaa aac gct tgg atc aaa tgc gcc aaa ctg ttg agg aaa agc tgg	384
Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp	
115 120 125	
aaa aaa cgc tac aaa cgc gtt gca aac ttc ttt gaa act gta tcg cgt	432
Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg	
130 135 140	
caa cta gag agc gtc aat caa ggt ctg ggt aga tgg aaa ctg tgc caa	480
Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln	
145 150 155 160	
gat gtt ggt acc act gaa caa agt ctg tca aat act aag aca agg gga	528
Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly	
165 170 175	
ata tta ggg gag tta caa ctg ggt caa att ata gaa gat att atg aca	576
Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr	
180 185 190	

gtt agt caa tat gag aga gaa ttt cct acg gtg tct ggc tct tct gag 624
 Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu
 195 200 205

cgt gtt gaa tat gct att aaa tac ctg gaa atg gtc agg gag att ata 672
 Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile
 210 215 220

tct att tgc cta ttg act cta agt ttc tct aga aga tta tta ccg att 720
 Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile
 225 230 235 240

ggg aga tgc tta tgg aat tgg gtg acc agg ttc aaa tgg aac tct att 768
 Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile
 245 250 255

cgt aat ctt tac tgg gca agt att cgt aaa ttt gca aaa gat ata aac 816
 Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn
 260 265 270

aat aag tac tta aat cct cct gaa acg aca aat ttt ggt atc atg ttc 864
 Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

tta cca act gaa ggg ctc tat tct gaa gtg gta aga aat gca aca ttc 912
 Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
 290 295 300

ttt gat agt cta aga cgt gac gaa aat att gta gta gct gga ccg tca 960
 Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
 305 310 315 320

acc tta tct gct tac taa 978
 Thr Leu Ser Ala Tyr
 325

<210> 21

<211> 325

<212> PRT

<213> group B streptococcus

<400> 21

Met Leu Val Ile Ile Leu Ile Ile Val Leu Ala Ser Leu Thr Val Thr
 1 5 10 15

Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys
 20 25 30

Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln
 35 40 45
 Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn
 50 55 60
 Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn
 65 70 75 80
 Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu
 85 90 95
 Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser
 100 105 110
 Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp
 115 120 125
 Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg
 130 135 140
 Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln
 145 150 155 160
 Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly
 165 170 175
 Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr
 180 185 190
 Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu
 195 200 205
 Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile
 210 215 220
 Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile
 225 230 235 240
 Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile
 245 250 255
 Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn
 260 265 270
 Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
290 295 300

Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
305 310 315 320

Thr Leu Ser Ala Tyr
325

<210> 22

<211> 579

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(579)

<400> 22

atg cga aaa gaa gtg aca cca gag atg ctt aac tat aat aag tat cct 48
Met Arg Lys Glu Val Thr Pro Glu Met Leu Asn Tyr Asn Lys Tyr Pro
1 5 10 15

ggc cca cag ttt att cac ttt gaa aat atc gtt aaa agt gat gat att 96
Gly Pro Gln Phe Ile His Phe Glu Asn Ile Val Lys Ser Asp Asp Ile
20 25 30

gaa ttt caa ctt gtt att aat gaa aaa tca gct ttt gat gtg act gtc 144
Glu Phe Gln Leu Val Ile Asn Glu Lys Ser Ala Phe Asp Val Thr Val
35 40 45

ttt gga caa cgt ttt tct gag att tta tta aaa tat gat ttt atc gtt 192
Phe Gly Gln Arg Phe Ser Glu Ile Leu Leu Lys Tyr Asp Phe Ile Val
50 55 60

ggc gat tgg ggt aac gag cag ttg agg cta aga ggc ttt tac aaa gat 240
Gly Asp Trp Gly Asn Glu Gln Leu Arg Leu Arg Gly Phe Tyr Lys Asp
65 70 75 80

gct agt acg att aga aaa aat agc cgg att tca cgt tta gaa gat tat 288
Ala Ser Thr Ile Arg Lys Asn Ser Arg Ile Ser Arg Leu Glu Asp Tyr
85 90 95

att aaa gag tat tgt aac ttt ggt tgt gct tat ttt gtg ttg gag aat 336
Ile Lys Glu Tyr Cys Asn Phe Gly Cys Ala Tyr Phe Val Leu Glu Asn

100	105	110	
cca aat cct aga gat att aaa ttt gat gat gaa aga cct cat aag cgt			384
Pro Asn Pro Arg Asp Ile Lys Phe Asp Asp Glu Arg Pro His Lys Arg			
115	120	125	
cgt aag tca aga tcc aaa tca caa tca tca aag tca caa act aga aat			432
Arg Lys Ser Arg Ser Lys Ser Gln Ser Ser Lys Ser Gln Thr Arg Asn			
130	135	140	
aat cgt tcc cag tca aat gcc aat gct cat ttt aca agt aaa aag cgt			480
Asn Arg Ser Gln Ser Asn Ala Asn Ala His Phe Thr Ser Lys Lys Arg			
145	150	155	160
aaa gac aca aaa cgc cgt caa gaa cgt cat att aaa gaa gag caa gat			528
Lys Asp Thr Lys Arg Arg Gln Glu Arg His Ile Lys Glu Glu Gln Asp			
165	170	175	
aag gaa atg acc tct gca aag cag cat ttg tta ttc gta aga aaa aat			576
Lys Glu Met Thr Ser Ala Lys Gln His Leu Leu Phe Val Arg Lys Asn			
180	185	190	
taa			579
<210> 23			
<211> 192			
<212> PRT			
<213> group B streptococcus			
<400> 23			
Met Arg Lys Glu Val Thr Pro Glu Met Leu Asn Tyr Asn Lys Tyr Pro			
1	5	10	15
Gly Pro Gln Phe Ile His Phe Glu Asn Ile Val Lys Ser Asp Asp Ile			
20	25	30	
Glu Phe Gln Leu Val Ile Asn Glu Lys Ser Ala Phe Asp Val Thr Val			
35	40	45	
Phe Gly Gln Arg Phe Ser Glu Ile Leu Leu Lys Tyr Asp Phe Ile Val			
50	55	60	
Gly Asp Trp Gly Asn Glu Gln Leu Arg Leu Arg Gly Phe Tyr Lys Asp			
65	70	75	80
Ala Ser Thr Ile Arg Lys Asn Ser Arg Ile Ser Arg Leu Glu Asp Tyr			

85

90

95

Ile Lys Glu Tyr Cys Asn Phe Gly Cys Ala Tyr Phe Val Leu Glu Asn
 100 105 110

Pro Asn Pro Arg Asp Ile Lys Phe Asp Asp Glu Arg Pro His Lys Arg
 115 120 125

Arg Lys Ser Arg Ser Lys Ser Gln Ser Ser Lys Ser Gln Thr Arg Asn
 130 135 140

Asn Arg Ser Gln Ser Asn Ala Asn Ala His Phe Thr Ser Lys Lys Arg
 145 150 155 160

Lys Asp Thr Lys Arg Arg Gln Glu Arg His Ile Lys Glu Glu Gln Asp
 165 170 175

Lys Glu Met Thr Ser Ala Lys Gln His Leu Leu Phe Val Arg Lys Asn
 180 185 190

<210> 24

<211> 609

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(609)

<400> 24

atg aca ata aaa aaa gtg tta agt gta aca gga att att tta gtg aca 48
 Met Thr Ile Lys Lys Val Leu Ser Val Thr Gly Ile Ile Leu Val Thr
 1 5 10 15

gta gcg tct cta gct gct tgt agc tca aaa tct cat act act aag acg 96
 Val Ala Ser Leu Ala Ala Cys Ser Ser Lys Ser His Thr Thr Lys Thr
 20 25 30

ggc aaa aaa gaa gtt aat ttt gca act gtt gga aca acg gca cct ttt 144
 Gly Lys Lys Glu Val Asn Phe Ala Thr Val Gly Thr Thr Ala Pro Phe
 35 40 45

tct tat gtg aag gat ggg aaa ctg act ggc ttt gat att gaa gta gcc 192
 Ser Tyr Val Lys Asp Gly Lys Leu Thr Gly Phe Asp Ile Glu Val Ala
 50 55 60

aaa gct gtt ttt aaa ggt tca gat aac tat aaa gtc act ttt aaa aaa 240
 Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys
 65 70 75 80

aca gaa tgg tca tcg gta ttt acc ggc att gat tca gga aag ttt caa 288
 Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln
 85 90 95

atg ggt gga aat aat att tct tat tca tca gag aga tct caa aaa tay 336
 Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr
 100 105 110

tta ttt tca tac cca ata ggc tct act cct tca gtt tta gca gtt cct 384
 Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro
 115 120 125

aag aat agt aat atc aaa gct tat aat gat att agt ggt cat aaa aca 432
 Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr
 130 135 140

cag gtt gtc caa gga acg aca act gcc aag caa tta gaa aat ttc aat 480
 Gln Val Val Gln Gly Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn
 145 150 155 160

aaa gag cat cag aaa aat cct gtt act cta aaa tat act aat gaa aat 528
 Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
 165 170 175

att aca cag att cta acg aat ttg agt gat gga aaa gct gat ttt aaa 576
 Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
 180 185 190

ctt ttg acg gac caa ctg tta acg cta tta taa 609
 Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
 195 200

<210> 25

<211> 202

<212> PRT

<213> group B streptococcus

<400> 25

Met Thr Ile Lys Lys Val Leu Ser Val Thr Gly Ile Ile Leu Val Thr
 1 5 10 15

Val Ala Ser Leu Ala Ala Cys Ser Ser Lys Ser His Thr Thr Lys Thr
 20 25 30

Gly Lys Lys Glu Val Asn Phe Ala Thr Val Gly Thr Thr Ala Pro Phe
35 40 45

Ser Tyr Val Lys Asp Gly Lys Leu Thr Gly Phe Asp Ile Glu Val Ala
50 55 60

Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys
65 70 75 80

Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln
85 90 95

Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr
100 105 110

Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro
115 120 125

Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr
130 135 140

Gln Val Val Gln Gly Thr Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn
145 150 155 160

Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
165 170 175

Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
180 185 190

Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
195 200

<210> 26

<211> 357

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(357)

<400> 26

atg aag aat ata aca aag cta tca act gtt gct tta agc cta cta ctt 48
Met Lys Asn Ile Thr Lys Leu Ser Thr Val Ala Leu Ser Leu Leu Leu

1	5	10	15	
tgt acg gcg tgt gct gca tca aac acg tct aca tct aaa aca cag tct				96
Cys Thr Ala Cys Ala Ala Ser Asn Thr Ser Thr Ser Lys Thr Gln Ser				
20	25	30		
cat cat cct aaa caa act aaa ctc aca gat aag caa aaa gaa gaa ccc				144
His His Pro Lys Gln Thr Lys Leu Thr Asp Lys Gln Lys Glu Glu Pro				
35	40	45		
aaa aac aaa gaa gct gct gat caa gag atg cat ccc caa ggc gct gtt				192
Lys Asn Lys Glu Ala Ala Asp Gln Glu Met His Pro Gln Gly Ala Val				
50	55	60		
gat ttg aca aaa tat aag gca aaa ccg gtc aaa gat tat gga aaa aaa				240
Asp Leu Thr Lys Tyr Lys Ala Lys Pro Val Lys Asp Tyr Gly Lys Lys				
65	70	75	80	
atc gat gtt ggt gat ggc aag aaa atg aac att tat gaa act ggt cag				288
Ile Asp Val Gly Asp Gly Lys Lys Met Asn Ile Tyr Glu Thr Gly Gln				
85	90	95		
gga aaa att cca att gtt ttt att cct ggt caa gct gag att cgc cac				336
Gly Lys Ile Pro Ile Val Phe Ile Pro Gly Gln Ala Glu Ile Arg His				
100	105	110		
gct atg ctt ata aga att taa				357
Ala Met Leu Ile Arg Ile				
115				
 <210> 27				
<211> 118				
<212> PRT				
<213> group B streptococcus				
 <400> 27				
Met Lys Asn Ile Thr Lys Leu Ser Thr Val Ala Leu Ser Leu Leu Leu				
1	5	10	15	
Cys Thr Ala Cys Ala Ala Ser Asn Thr Ser Thr Ser Lys Thr Gln Ser				
20	25	30		
His His Pro Lys Gln Thr Lys Leu Thr Asp Lys Gln Lys Glu Glu Pro				
35	40	45		
Lys Asn Lys Glu Ala Ala Asp Gln Glu Met His Pro Gln Gly Ala Val				
50	55	60		

Asp Leu Thr Lys Tyr Lys Ala Lys Pro Val Lys Asp Tyr Gly Lys Lys
65 70 75 80

Ile Asp Val Gly Asp Gly Lys Lys Met Asn Ile Tyr Glu Thr Gly Gln
85 90 95

Gly Lys Ile Pro Ile Val Phe Ile Pro Gly Gln Ala Glu Ile Arg His
100 105 110

Ala Met Leu Ile Arg Ile
115

<210> 28

<211> 1191

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(1191)

<400> 28

gtg aat gaa tcg acc atc aga aaa gaa ttt aaa ata gtt gtt ttt aaa 48
Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
1 5 10 15

tgg atc tta aat aat caa gca gtt att gct ctc atg att acc ttt ttg 96
Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
20 25 30

gta ttt tta acg att ttt att ttt acc aaa atc tct ttt atg ttt aaa 144
Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys
35 40 45

cct gtg ttt gat ttt ctt gct gtg ctg ata ttg ccg ctt gta att tct 192
Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser
50 55 60

ggc ttg ctt tat tac cta tta aaa cct atg gtt aca ttt tta gag aag 240
Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys
65 70 75 80

cgg gga att aag cgt gta aca gcg ata tta tca gtt ttt act att ata 288
Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile
85 90 95

atc ctt ctg tta att tgg gca atg tct agt ttt att ccc atg atg agt 336
 Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser
 100 105 110

aat caa tta cgc cat ttt atg gaa gat ctc cct tca tat gtg aat aaa 384
 Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys
 115 120 125

gtg caa atg gaa aca agt tcg ttt ata gat cac aac cct tgg tta aaa 432
 Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys
 130 135 140

tct tat aaa ggg gaa ata tcg agc atg tta tct aat atc agt agc caa 480
 Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln
 145 150 155 160

gcg gtc tct tat gct gaa aaa ttt tca aag aat gtt tta gat tgg gca 528
 Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala
 165 170 175

gga aat tta gct agt aca gtt gca cgt gtg aca gta gca aca atc atg 576
 Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met
 180 185 190

gct ccc ttt att ttg ttt tat ctt tta aga gat agt cgc aac atg aag 624
 Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys
 195 200 205

aat ggt ttc tta atg gtt tta cca acc aaa cta cgc caa cca gct gat 672
 Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp
 210 215 220

cgt att ttg cga gaa atg aat agt caa atg tca gga tat gtg caa gga 720
 Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly
 225 230 235 240

caa atc att gtt gct att act gtt ggt gtt att ttt tca ata atg tat 768
 Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr
 245 250 255

agt att ata ggc ctt aga tat ggc gtg aca tta ggg att att gcc ggt 816
 Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly
 260 265 270

gtg tta aat atg gtt ccc tat ttg gga agt ttt gtc gcc caa att cca 864
 Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro
 275 280 285

gtg ttt atc tta gcg ctt gtc gca gga cct gtt atg gtt gtt aaa gtt 912
 Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val
 290 295 300

gcg att gtt ttt gtt att gag caa act cta gag gga cgc ttt gtc tca 960
 Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser
 305 310 315 320

cct ttg gtt tta ggt aat aaa ctt agc att cat cca att aca att atg 1008
 Pro Leu Val Leu Gly Asn Lys Leu Ser Ile His Pro Ile Thr Ile Met
 325 330 335

ttt att tta tta acc tct gga gcg atg ttt ggt gtt tgg gga gta ttc 1056
 Phe Ile Leu Leu Thr Ser Gly Ala Met Phe Gly Val Trp Gly Val Phe
 340 345 350

ctc agt att ccg att tat gca tct atc aaa gtt gtt gtt aaa gaa ttg 1104
 Leu Ser Ile Pro Ile Tyr Ala Ser Ile Lys Val Val Val Lys Glu Leu
 355 360 365

ttt gat tgg tac aaa gct gtc agt ggg cta tat aca ata gat gtt gtt 1152
 Phe Asp Trp Tyr Lys Ala Val Ser Gly Leu Tyr Thr Ile Asp Val Val
 370 375 380

act gaa gaa aga agt gaa gaa gtt aaa aat gtt gaa tag 1191
 Thr Glu Glu Arg Ser Glu Glu Val Lys Asn Val Glu
 385 390 395

<210> 29

<211> 396

<212> PRT

<213> group B streptococcus

<400> 29

Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
 1 5 10 15

Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
 20 25 30

Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys
 35 40 45

Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser
 50 55 60

Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys
65 70 75 80

Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile
85 90 95

Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser
100 105 110

Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys
115 120 125

Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys
130 135 140

Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln
145 150 155 160

Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala
165 170 175

Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met
180 185 190

Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys
195 200 205

Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp
210 215 220

Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly
225 230 235 240

Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr
245 250 255

Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly
260 265 270

Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro
275 280 285

Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val
290 295 300

Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser
305 310 315 320

Pro Leu Val Leu Gly Asn Lys Leu Ser Ile His Pro Ile Thr Ile Met
325 330 335

Phe Ile Leu Leu Thr Ser Gly Ala Met Phe Gly Val Trp Gly Val Phe
340 345 350

Leu Ser Ile Pro Ile Tyr Ala Ser Ile Lys Val Val Val Lys Glu Leu
355 360 365

Phe Asp Trp Tyr Lys Ala Val Ser Gly Leu Tyr Thr Ile Asp Val Val
370 375 380

Thr Glu Glu Arg Ser Glu Glu Val Lys Asn Val Glu
385 390 395

<210> 30

<211> 1230

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(1230)

<400> 30

atg ttt atg gga atc cca caa tat ttc ttc tac ctt atc tta gct gtc 48
Met Phe Met Gly Ile Pro Gln Tyr Phe Phe Tyr Leu Ile Leu Ala Val
1 5 10 15

cta cca att tac atc ggc tta ttc ttt aag aag cgt ttt gcc tta tat 96
Leu Pro Ile Tyr Ile Gly Leu Phe Phe Lys Lys Arg Phe Ala Leu Tyr
20 25 30

gag att att ttt agt cta agt ttt att gta atg atg ttg act ggt agt 144
Glu Ile Ile Phe Ser Leu Ser Phe Ile Val Met Met Leu Thr Gly Ser
35 40 45

act ttt aat caa ttg aag tca cta ttg gca tac gtt gtc gga cag tct 192
Thr Phe Asn Gln Leu Lys Ser Leu Leu Ala Tyr Val Val Gly Gln Ser
50 55 60

ctg cta gtt ttt atc tat aaa gct tac cgg aaa cga ttt aat cat act 240
Leu Leu Val Phe Ile Tyr Lys Ala Tyr Arg Lys Arg Phe Asn His Thr
65 70 75 80

ttg gtc ttt tat gta acg gtt tgt tta tct att ttt ccg cta ttt ttg 288

Leu Val Phe Tyr Val Thr Val Cys Leu Ser Ile Phe Pro Leu Phe Leu	
85 90 95	
gta aaa tta att cca gct ata tct gag gat ggg cat cag tca ctt ttt	336
Val Lys Leu Ile Pro Ala Ile Ser Glu Asp Gly His Gln Ser Leu Phe	
100 105 110	
ggg ttt cta gga att tct tac ctt act ttt aga gct gtt gct atg att	384
Gly Phe Leu Gly Ile Ser Tyr Leu Thr Phe Arg Ala Val Ala Met Ile	
115 120 125	
att gaa atg aga gac ggt gtc ttg aaa gaa ttt act tta tgg gaa ttc	432
Ile Glu Met Arg Asp Gly Val Leu Lys Glu Phe Thr Leu Trp Glu Phe	
130 135 140	
tta aga ttt tta ctc ttc ttt cca act ttc tca agt gga cca att gat	480
Leu Arg Phe Leu Leu Phe Phe Pro Thr Phe Ser Ser Gly Pro Ile Asp	
145 150 155 160	
cgt ttt aaa cga ttc aat gag gat tac att aat atc cca gat cga aac	528
Arg Phe Lys Arg Phe Asn Glu Asp Tyr Ile Asn Ile Pro Asp Arg Asn	
165 170 175	
gaa ctc cta gat atg tta ggt caa gcg att cat tat ttg atg tta ggt	576
Glu Leu Leu Asp Met Leu Gly Gln Ala Ile His Tyr Leu Met Leu Gly	
180 185 190	
ttt ctc tat aag ttt att tta gcc tat att ttt gga agt ctg att atg	624
Phe Leu Tyr Lys Phe Ile Leu Ala Tyr Ile Phe Gly Ser Leu Ile Met	
195 200 205	
cct cct cta aaa gaa tta gcg cta gaa cag ggt ggt gtg ttt aat tgg	672
Pro Pro Leu Lys Glu Leu Ala Leu Glu Gln Gly Gly Val Phe Asn Trp	
210 215 220	
cca aca ctt ggg gtt atg tat gcc ttt ggt ttt gat ttg ttc ttt gat	720
Pro Thr Leu Gly Val Met Tyr Ala Phe Gly Phe Asp Leu Phe Phe Asp	
225 230 235 240	
ttt gca ggt tac aca atg ttt gcg ttg gct att tct aac cta atg ggg	768
Phe Ala Gly Tyr Thr Met Phe Ala Leu Ala Ile Ser Asn Leu Met Gly	
245 250 255	
att aag tct ccg att aac ttt gac aaa cct ttc aaa tca cgc gac cta	816
Ile Lys Ser Pro Ile Asn Phe Asp Lys Pro Phe Lys Ser Arg Asp Leu	
260 265 270	
aaa gaa ttt tgg aat aga tgg cat atg agc ctt tct ttc tgg ttt aga	864

Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg
 275 280 285
 gac ttt gtt ttc atg agg ctt gtt aag ctt tta gtt aaa aat aaa gtt 912
 Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val
 290 295 300
 ttt aaa aac cgt aat gtt act tca agt gta gct tat att atc aat atg 960
 Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
 305 310 315 320
 ctt ctt atg gga ttc tgg cat ggg tta act tgg tac tat ata gcc tat 1008
 Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
 325 330 335
 ggt ctc ttt cat ggg att ggc cta gtt att aat gac gct tgg gta cgt 1056
 Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
 340 345 350
 aag aag aaa aat ayt aat aaa gaa aga aga ttg gct aaa aaa cca ctt 1104
 Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
 355 360 365
 tta cca gaa aac aaa tgg act tat gct ttg ggt gtc ttc atc acc ttt 1152
 Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
 370 375 380
 aat gta gtt atg ttt tct ttc ttg att ttt tca gga ttt tta gat ctt 1200
 Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
 385 390 395 400
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<211> 409

<212> PRT

<213> group B streptococcus

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Leu Pro Ile Tyr Ile Gly Leu Phe Phe Lys Lys Arg Phe Ala Leu Tyr
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Glu Ile Ile Phe Ser Leu Ser Phe Ile Val Met Met Leu Thr Gly Ser
 35 40 45
 Thr Phe Asn Gln Leu Lys Ser Leu Leu Ala Tyr Val Val Gly Gln Ser
 50 55 60
 Leu Leu Val Phe Ile Tyr Lys Ala Tyr Arg Lys Arg Phe Asn His Thr
 65 70 75 80
 Leu Val Phe Tyr Val Thr Val Cys Leu Ser Ile Phe Pro Leu Phe Leu
 85 90 95
 Val Lys Leu Ile Pro Ala Ile Ser Glu Asp Gly His Gln Ser Leu Phe
 100 105 110
 Gly Phe Leu Gly Ile Ser Tyr Leu Thr Phe Arg Ala Val Ala Met Ile
 115 120 125
 Ile Glu Met Arg Asp Gly Val Leu Lys Glu Phe Thr Leu Trp Glu Phe
 130 135 140
 Leu Arg Phe Leu Leu Phe Phe Pro Thr Phe Ser Ser Gly Pro Ile Asp
 145 150 155 160
 Arg Phe Lys Arg Phe Asn Glu Asp Tyr Ile Asn Ile Pro Asp Arg Asn
 165 170 175
 Glu Leu Leu Asp Met Leu Gly Gln Ala Ile His Tyr Leu Met Leu Gly
 180 185 190
 Phe Leu Tyr Lys Phe Ile Leu Ala Tyr Ile Phe Gly Ser Leu Ile Met
 195 200 205
 Pro Pro Leu Lys Glu Leu Ala Leu Glu Gln Gly Gly Val Phe Asn Trp
 210 215 220
 Pro Thr Leu Gly Val Met Tyr Ala Phe Gly Phe Asp Leu Phe Phe Asp
 225 230 235 240
 Phe Ala Gly Tyr Thr Met Phe Ala Leu Ala Ile Ser Asn Leu Met Gly
 245 250 255
 Ile Lys Ser Pro Ile Asn Phe Asp Lys Pro Phe Lys Ser Arg Asp Leu
 260 265 270
 Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg
 275 280 285

Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val
 290 295 300

Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
 305 310 315 320

Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
 325 330 335

Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
 340 345 350

Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
 355 360 365

Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
 370 375 380

Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
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Leu Trp Phe Pro Gln Pro His Asn Lys
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tgc gtt gga tgt tct gcc aat aaa gat aat caa aaa act aaa act gag 96
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gat c 100
 Asp

<210> 33
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Asp

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 Glu Tyr Gly Leu Gly Val Ser Thr Gly Leu Asp Leu Pro Glu Ser Glu
 20 25 30
 ggt tat gta cct gga aaa tac agc tta gga aca act cta atg gaa tcg 144
 Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu Met Glu Ser
 35 40 45
 ttc ggt cag tat gat gcc tat aca cca atg caa ctt ggt cag tat atc 192
 Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly Gln Tyr Ile
 50 55 60
 tca act att gcg aat aat ggg aat cgt tta gca cct cac gtg gtt tca 240
 Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His Val Val Ser
 65 70 75 80
 gat atc tat gaa ggg aat gat tct aat aag ttc gct caa ttg gtt cgt 288

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Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln Leu Val Arg
      85                      90                      95

tca atc act cct aaa aca cta aat aag ata gct atc tca gat caa gag   336
Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
      100                      105                      110

tta gcc att att caa gaa ggt ttt tat aac gtt gtc aat agt gga agt   384
Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
      115                      120                      125

ggc tat gca act ggt acg tca atg agg ggg aat gtg aca acc att agy   432
Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Xaa
      130                      135                      140

ggt aaa act ggt acc gct gaa aca ttt gct aaa aat ata aat gga caa   480
Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
      145                      150                      155                      160

aca gtt tct acc tac aac tta aac gct att gcc tac gat act aat cgt   528
Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
      165                      170                      175

aaa ata gca gta gcg gta atg tat ccg cat gtt aca act gat aca aca   576
Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
      180                      185                      190

aaa tcc cat caa tta gtt gca cga gat atg att gat caa tat att tca   624
Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
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cag tca cag gac aat aag aga gga cat tga                               654
Gln Ser Gln Asp Asn Lys Arg Gly His
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<212> PRT

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Glu Tyr Gly Leu Gly Val Ser Thr Gly Leu Asp Leu Pro Glu Ser Glu
      20                      25                      30

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Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu Met Glu Ser
35 40 45

Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly Gln Tyr Ile
50 55 60

Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His Val Val Ser
65 70 75 80

Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln Leu Val Arg
85 90 95

Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
100 105 110

Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
115 120 125

Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Xaa
130 135 140

Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
145 150 155 160

Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
165 170 175

Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
180 185 190

Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
195 200 205

Gln Ser Gln Asp Asn Lys Arg Gly His
210 215